Figure 1A

```
   1  CCAATAACAACCGGGGCGTTCACCTTCGGATTTAGCAAGGTTTTGAAAAACTATTTAGGT   60

  61  GCCCATAAAAGGTCCCCTTCAGGTACCGGTCCGAAATTCCGGGTCAACCCAGGGTCCGGA  120

 121  TCAATTAAGGGTCTGGGGGGTGGCCACCTGGCCACTTTGGAAAATTGCAAGCATTTCCAA  180

 181  GCTTCATCCGGCTCCAGGGTTGGCCTCTCCAAAAGGCAGGCGGCTTTTAAACGGGTTCCA  240

 241  ACAGAAAGGACCTCCCTTGGTCTCCTCAATTCCTGGCTGGAGTTTCTCTTCTCGTGTTGT  300

 301  GGAAGGATTCCAAACCCACACACACAGGACCCGCATCCTGGGTGATGAAGTCAGACACGC  360

 361  AGCAGCTGGGTGAGTGCTACGCTCAAGATAAGCATCTGTGCCATTGTGGGGACTCCCTGG  420

 421  GCTGCTCTGCACCCGGACACTTGCTCTGTCCCCGCCATGTACAACGGGTCGTGCTGCCGC  480
   1                                        M  Y  N  G  S  ■  C  R    8

 481  ATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCGCTGCTCATTGTGGCCTTTGTGCTG  540
   9  I  E  G  D  T  I  S  Q  V  M  P  P  L  L  I  V  A  F  V  L   28

 541  GGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTCTGCTTCCACATGAAGACCTGGAAG  600
  29  G  A  L  G  N  G  V  A  L  C  G  F  C  F  H  M  K  T  W  K   48

 601  CCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCTGATTTCCTCCTTATGATCTGCCTG  660
  49  P  S  T  V  Y  L  F  N  L  A  V  A  D  F  L  L  M  I  C  L   68

 661  CCTTTTCGGACAGACTATTACCTCAGACGTAGACACTGGGCTTTTGGGGACATTCCCTGC  720
  69  P  F  R  T  D  Y  Y  L  R  R  R  H  W  A  F  G  D  I  P  C   88

 721  CGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCCGGGAGCATCGTGTTCCTTACGGTG  780
  89  R  V  G  L  F  T  L  A  M  N  R  A  G  S  I  V  F  L  T  V  108

 781  GTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCCCACCACGCGGTGAACACTATCTCC  840
 109  V  A  A  D  R  Y  F  K  V  V  H  P  H  H  A  V  N  T  I  S  128

 841  ACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGGGCCCTGGTCATCCTGGGAACAGTG  900
 129  T  R  V  A  A  G  I  V  C  T  L  W  A  L  V  I  L  G  T  V  148

 901  TATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAGACGGCCGTCTCCTGTGAGAGCTTC  960
 149  Y  L  L  L  E  N  H  L  C  V  Q  E  T  A  V  S  C  E  S  F  168
```

Figure 1B

```
 961  ATCATGGAGTCGGCCAATGGCTGGCATGACATCATGTTCCAGCTGGAGTTCTTTATGCCC  1020
 169  I  M  E  S  A  N  G  W  H  D  I  M  F  Q  L  E  F  F  M  P    188

1021  CTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTTTGGAGCCTGAGGCGGAGGCAGCAG  1080
 189  L  G  I  I  L  F  C  S  F  K  I  V  W  S  L  R  R  R  Q  Q    208

1081  CTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGGTTCATCATGGTGGTGGCAATTGTG  1140
 209  L  A  R  Q  A  R  M  K  K  A  T  R  F  I  M  V  V  A  I  V    228

1141  TTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGACTCTATTTCCTCTGGACGGTGCCC  1200
 229  F  I  T  C  Y  L  P  S  V  S  A  R  L  Y  F  L  W  T  V  P    248

1201  TCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTGCACATAACCCTCAGCTTCACCTAC  1260
 249  S  S  A  C  D  P  S  V  H  G  A  L  H  I  T  L  S  F  T  Y    268

1261  ATGAACAGCATGCTGGATCCCCTGGTGTATTATTTTTCAAGCCCCTCCTTTCCCAAATTC  1320
 269  M  N  S  M  L  D  P  L  V  Y  Y  F  S  S  P  S  F  P  K  F    288

1321  TACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAGCAGCCAGGACACTCAAAAACACAA  1380
 289  Y  N  K  L  K  I  C  S  L  K  P  K  Q  P  G  H  S  K  T  Q    308

1381  AGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGCAGGAGTTGCATCAGTGTGGCAAAA  1440
 309  R  P  E  E  M  P  I  S  N  L  G  R  R  S  C  I  S  V  A  K    328

1441  GTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCCCACTTGTTGAGTGGCACTGAACAAG  1500
 329  V  S  K  A  S  L  M  G  N  G  I  P  T  C                      342

1501  CAGACCAACAACACTGAGGAAGATAGAGTGGTGACTTAGAATTAACTCGTGCTAAGGGGT  1560

1561  CGGGGGCTTTGAAAATGCCACCCCCCTTTCTTATTGCAAGACGGCTTCTCGCACATGAAC  1620

1621  TGCATCCTTCTCATTCTGTCGGAAATGAAATTCACACAACTATACCTTTTGGGGAGGTTC  1680

1681  CAGTTGATTGAAGTGAGTTGGCTGCATTTTCTTATCTGATCACAATGGCAGGGGACAGAA  1740

1741  TGTGCATGGAGTGGAGCATGTGTGTGTTGGGAGGGGGGCTAGGAACTGCACAGCCCTTGT  1800

1801  GTAATTTTCGTTGTTTGTTTTTGTTTTGAGACAGAGTCTCACTCTGTGTCCCAGGCTGGA  1860

1861  GTGCAGTGGCACAGTCTCGGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCAATTCTCC  1920

1921  TGCCTCAGCCTCCCGAGTAGCTGGGATTAGAGGCGCCAGCCAACACACCCGGCTAATTTT  1980
```

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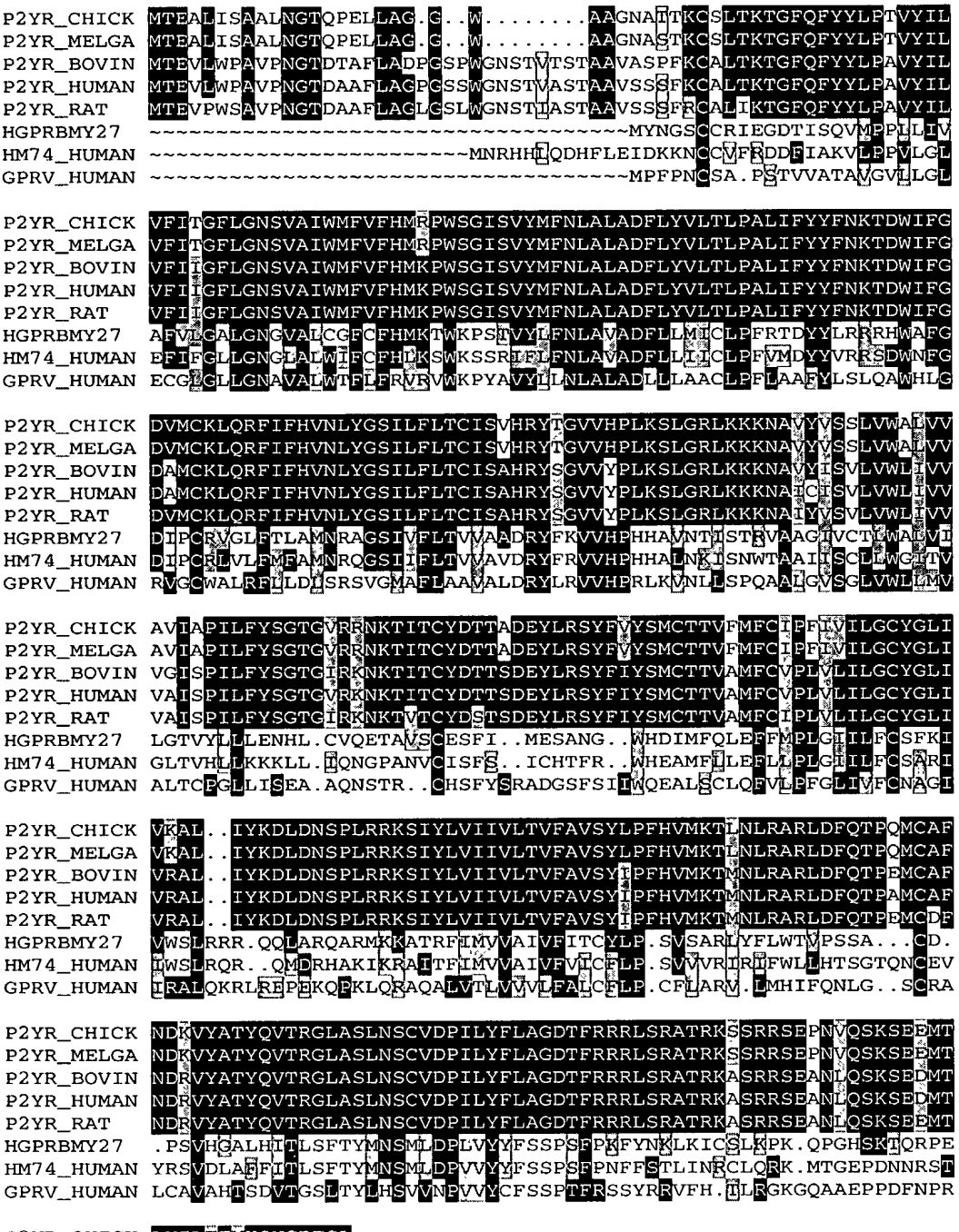
Figure 1C

```
1981  TGTATTTTTAGTAGAGACAGGGTTTTGCCATGTTGGCCAGGCTGGTCTCGAGCTCCTGAC  2040

2041  CTCAGGTGATCCGCCTGCCTTGGCCTCCCAAAGTGGTGGGATCACAGGCGTGAGCCACCG  2100

2101  TGCCCGGCCTCCCCTGTGTCATTTTAAATGGCTAAGTAAATGGGTATATGTGTTTGAATG  2160

2161  GGGCATGTTCACTCTCTTAGGGGCTATGGGGCAGTTAGCAGCATTTCCTATCCTCTGACC  2220

2221  TTAAATCATTCCTTATCTCAGAAAACAGAAACCGGGCTCAGTCAATCAATGCTTTATTTC  2280

2281  AGGCCGAATGAGGCTCTTTAGATTGGGATCTATTGATCTATCAATTTTCATCTTTACATT  2340

2341  TCTTTGTACATCTGTACATTTTGTCCAAATGTACATCTGTACGTCTGTCATCATTGTGAC  2400

2401  TTCCTGGTAGCCCAAGAAGAACAACAACAAAACAATCTGCTCTGACCTTCTTCAAATCTT  2460

2461  TGTATTTCAAAGAAGGTGCTGAGGGATCTGTTTCCTTGCCCTGGCTTCTCCAGTGGGATG  2520

2521  TGCTGAGTCCAATACAATTGCTTTTATAATTGCTTTTGAAAAAAAAAAAAAAAAAAAAG  2580
```

D0134 NP

Figure 2A

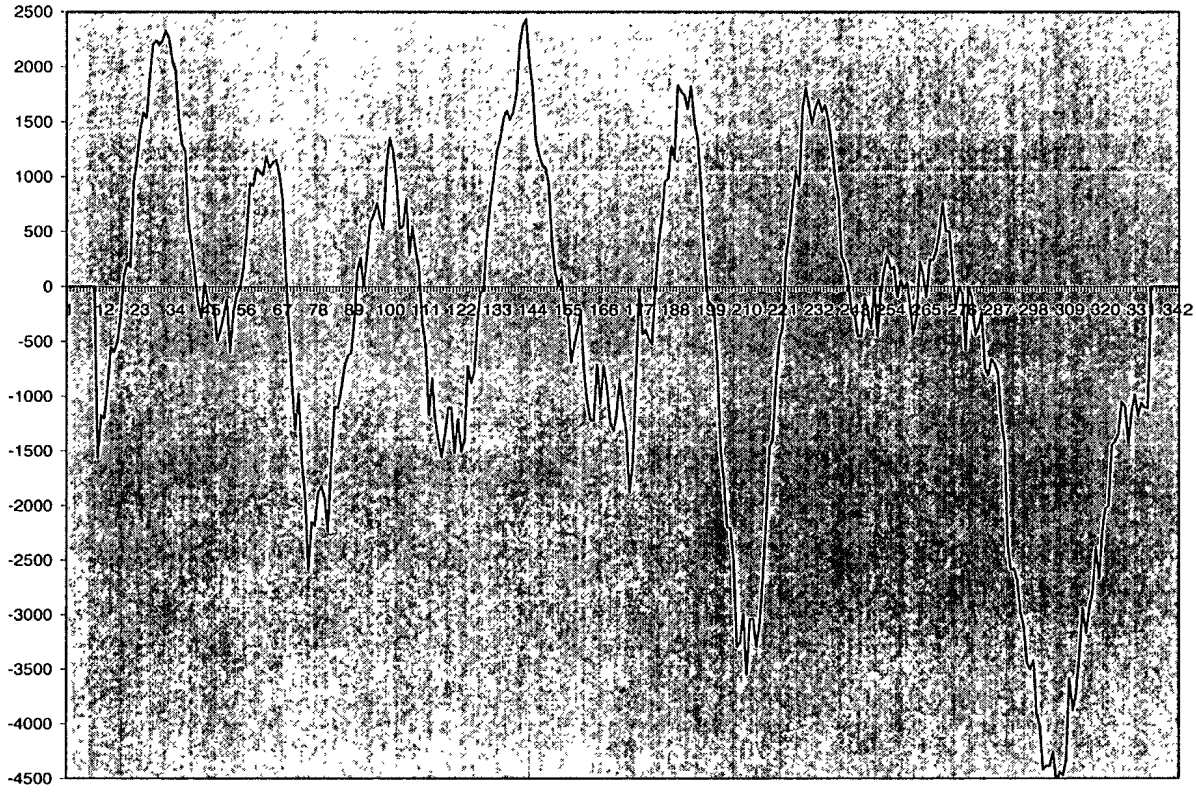


D0134 NP

Figure 2B

```
P2YR_CHICK ~~~~~
P2YR_MELGA ~~~~~
P2YR_BOVIN ~~~~~
P2YR_HUMAN ~~~~~
P2YR_RAT   ~~~~~
HGPRBMY27  ~~~~~
HM74_HUMAN GCCIE
GPRV_HUMAN ~~~~~
```

Figure 3


2500
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1500
1000
500
0
-500
-1000
-1500
-2000
-2500
-3000
-3500
-4000
-4500
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34
45
56
67
78
89
100
111
122
133
144
155
166
177
188
199
210
221
232
243
254
265
276
287
298
309
320
331
342

Figure 4

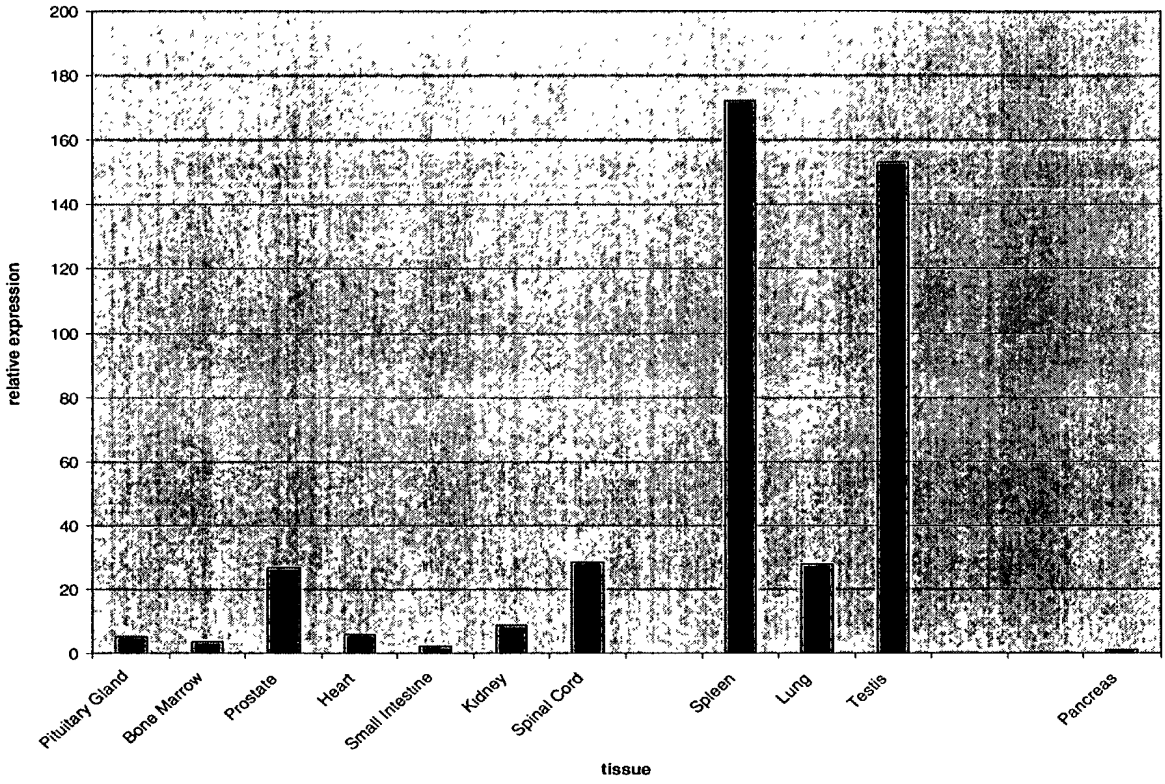
200
180
160
140
120
100
80
60
40
20
0
relative expression
Pituitary Gland
Bone Marrow
Prostate
Heart
Small Intestine
Kidney
Spinal Cord
Spleen
Lung
Testis
Pancreas
tissue

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Figure 5.

Protein	SWISS-PROT ID	Identities	Similarities
chicken P2Y purinoceptor 1 (ATP RECEPTOR) protein	P34996	28.9%	39.4%
turkey P2Y purinoceptor 1 (ATP RECEPTOR) protein	P49652	28.9%	39.4%
bovine P2Y purinoceptor 1 (ATP RECEPTOR) protein	P48042	28.7%	39.8%
human P2Y purinoceptor 1 (ATP RECEPTOR) protein	P47900	28.7%	39.5%
rat P2Y purinoceptor 1 (ATP RECEPTOR) protein	P49651	28.7%	39.8%
human G protein-coupled receptor, HM74 protein	P49019	53.6%	61.0%
human G protein-coupled receptor, GPR31 protein	O00270	33.0%	43.6%

10092137.030607

Figure 6

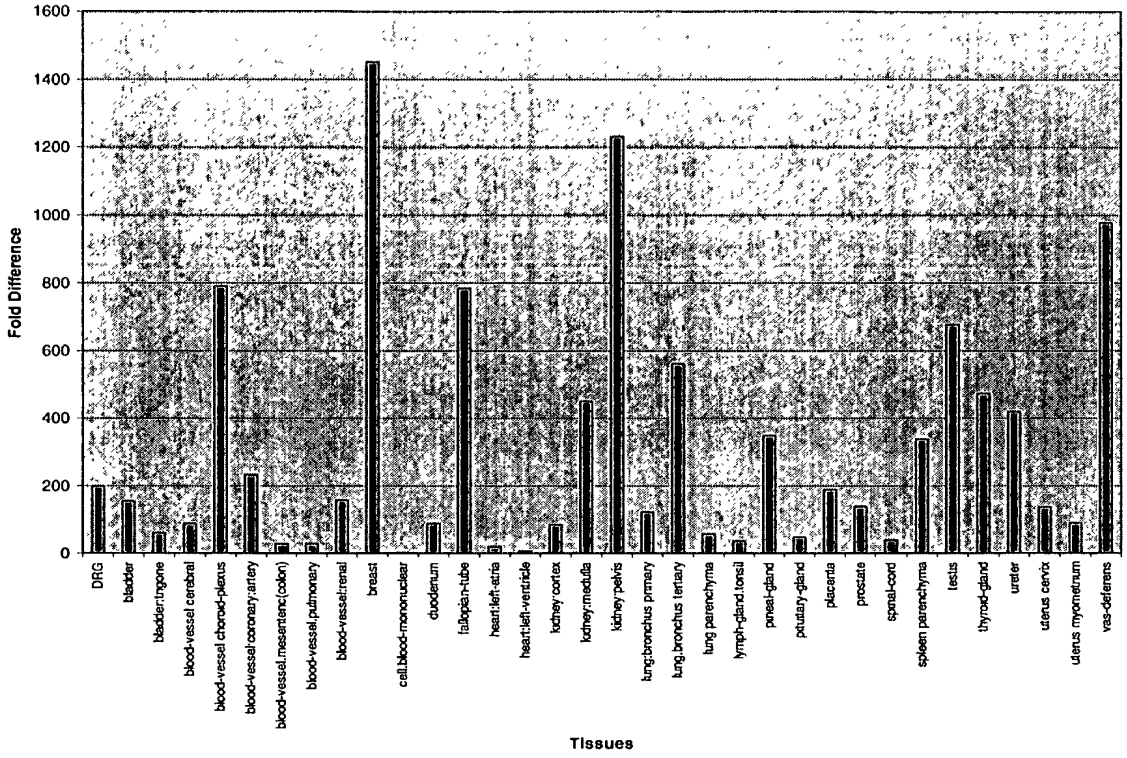


Figure 7

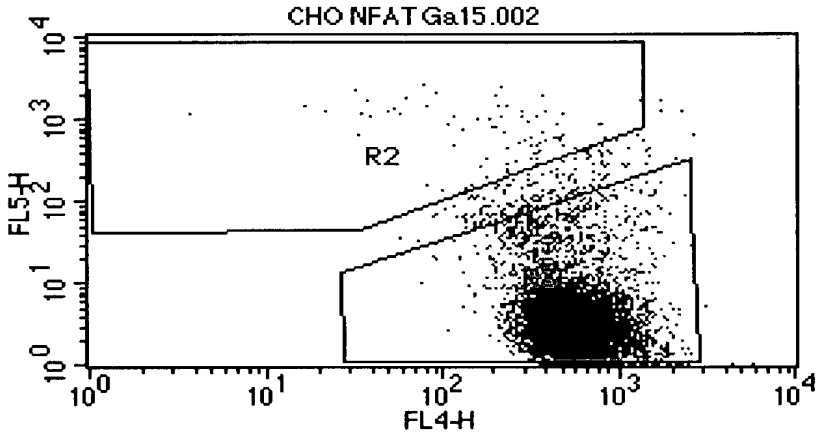
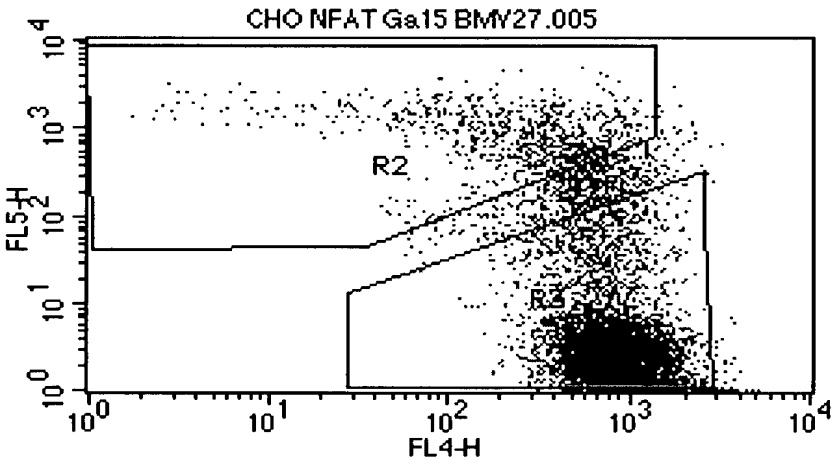
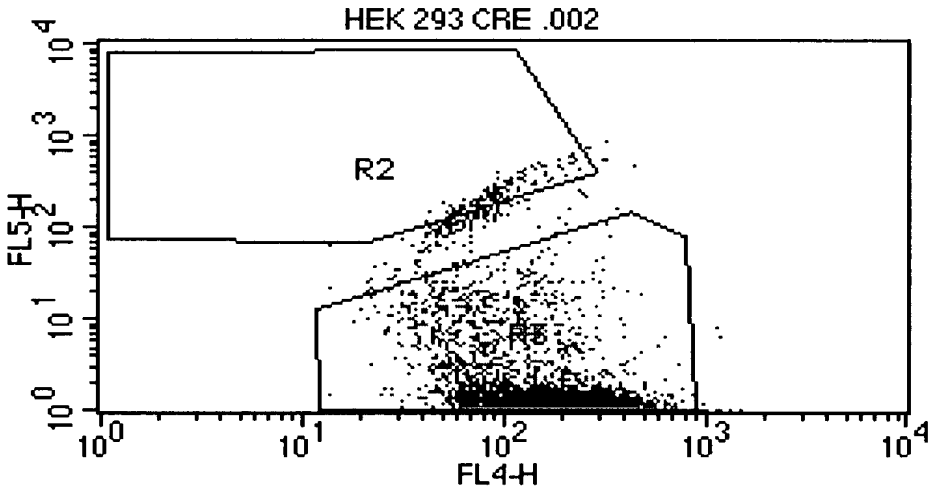


Figure 8



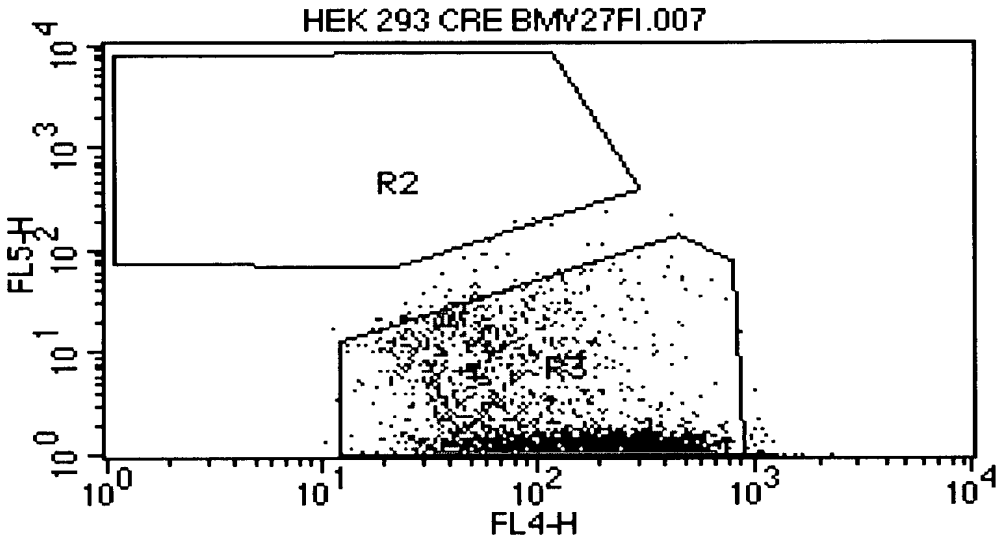
D0134 NP

Figure 9



D0134 NP

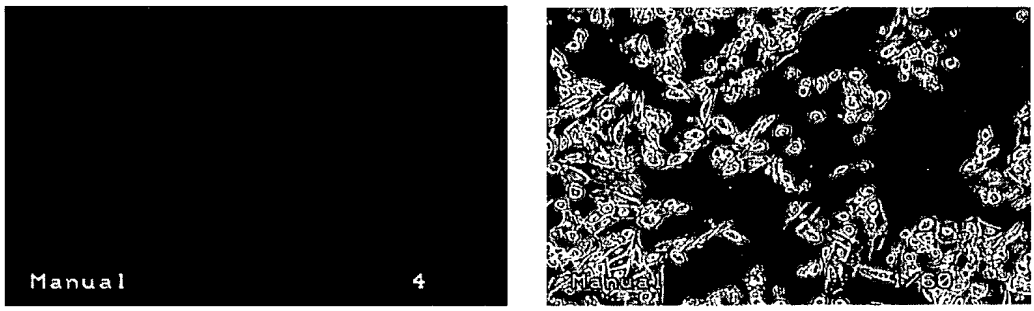
Figure 10



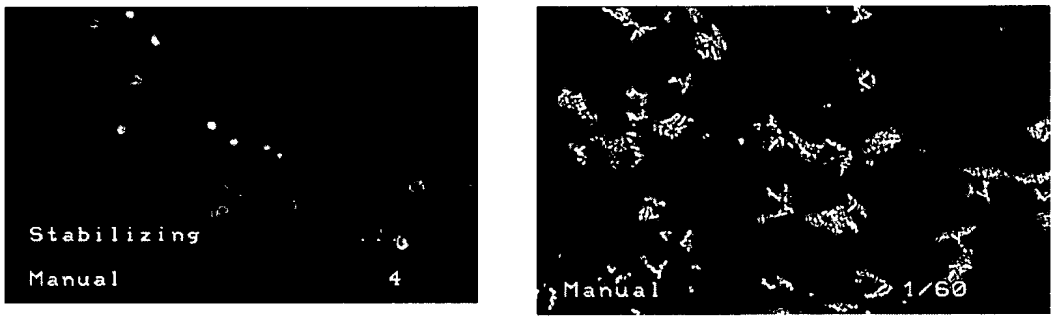
1009P135.030602

Figure 11

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)



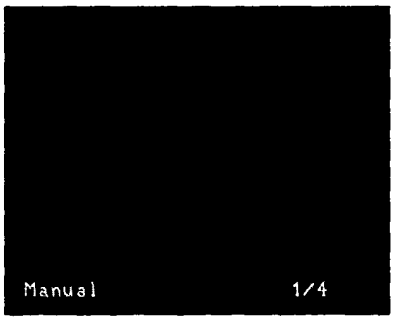
Cho NFAT Ga15 BMY27 (Fluorescent vs. Bright Field)



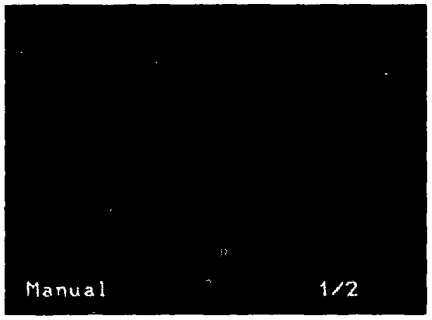
D0134 NP

Figure 12

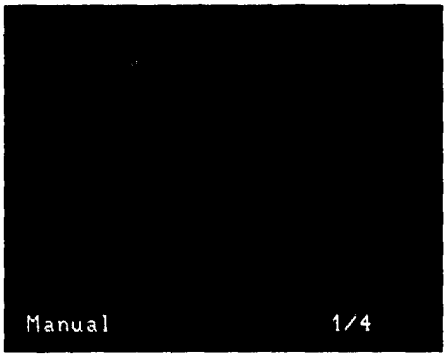
a. Cho NFAT Ga15



b. Cho NFAT Ga15 + T/P



c. Cho NFAT Ga15 oGPCR-Intermediate



d. Cho NFAT Ga15 oGPCR High